gi|12311218|emb|CAC22595.1| unnamed protein product [Hirudinaria manillensis] Length = 488 Score = 962 bits (2486), Expect = 0.0 Identities = 488/488 (100%), Positives = 488/488 (100%)  ${\tt KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFR\acute{V}~60}$ KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV 60 Sbict: 1 Query: 61 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG 120 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG Sbjct: 61 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG 120 Query: 121 SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180 SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS Sbjct: 121 SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180 Query: 181 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL 240 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL Sbict: 181 AHNLTEKOVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL 240

Query: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD 300 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD

Sbjct: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD 300

Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV

Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360

Query: 361 GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420 GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG

Sbjct: 361 GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420

Query: 421 KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD 480 KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD

Sbjct: 421 KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD 480

Query: 481 ANVEACKK 488 ANVEACKK Sbjct: 481 ANVEACKK 488

## >gi|12311214|emb|CAC22593.1| unnamed protein product [Hirudinaria manillensis] Length = 488

Score = 905 bits (2340), Expect = 0.0 Identities = 463/488 (94%), Positives = 471/488 (96%)

KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV 60 Query: 1 KEIAVTIDDKNVIAS S SF GVAFDASLFSPKG WSFV+ITSPKLFKLLEGLSPGYFRV

KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV 60 Sbict: 1 Query: 61 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG 120

GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFD+LVKLTKG Sbjct: 61 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG 120

Query: 121 SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180 SKMRLLFDLNAEVRTGYEIGKK TSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS

Sbjct: 121 SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180

Query: 181 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL 240 AHNLTEKQVGEDFKALHKVLEKYPTLNKGS VGPDVGWMGVS VKGLAD AGD VTAFTL

Sbjct: 181 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL 240

Query: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD 300 HQYYFDGNTSDVS YLDA+YFKKLQQLFDKVKDVLK+SPHKD+PLWLGETSSG NSGT+D

Sbjct: 241 HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED 300.

Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360

Query: 361 GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG 420 GNTVFKVDV DPTNK RVYAQCTKTNSKHTQ +YYKGSLTIFALNVGD +VTLKI QY G Sbjct: 361 GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG 420

Query: 421 KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD 480

Query: 481 ANVEACKK 488
ANVEACKK
Sbjct: 481 ANVEACKK 488

Score = 904 bits (2337), Expect = 0.0 Identities = 462/488 (94%), Positives = 471/488 (96%)

KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV 60 Query: 1 KEIAVTIDDKNVIAS SESFHGVAFDASLFSPKG WSFV+ITSPKLFKLLEGLSPGYFRV Sbjct: 1 KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV 60 Query: 61 GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG 120 GGTFAN LFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFD+LVKLTKG Sbjct: 61 GGTFANRLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG 120 Query: 121 SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180 SKMRLLFDLNAEVRTGYEIGKK TSTWDSSEAEKLFKYCVSKGYGDNIDWELGN PDHTS Sbjct: 121 SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNGPDHTS 180 Query: 181 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL 240 AHNLTEKQVGEDFKALHKVLEKYPTLNKGS VGPDVGWMGVSYVKGLAD AGD VTAFTL Sbjct: 181 AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSYVKGLADEAGDHVTAFTL 240 Query: 241 HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD 300 HQYYFDGNTSDVS YLDA+YFKKLQQLFDKVKDVLK+SPHKDKPLWLGETSSG NSGT+D Sbjct: 241 HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDKPLWLGETSSGYNSGTED 300 Query: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIY+GYYG LDKNTLEPNPDYWLMHVHNSLV Sbjct: 301 VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYSGYYGPLDKNTLEPNPDYWLMHVHNSLV 360 Query: 361 GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLT1FALNVGDEEVTLKIDQYGG 420 GNTVFKVDV DPTNK RVYAQCTKTNSKHTQ +YYKGSLTIFALNVGDE+VTLKI QY G Sbjct: 361 GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIGQYSG 420 Query: 421 KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD 480 KKIYSYILTPEGGQLTSQKVLLNGKELNL SDQLP+LNADESKTSFTLSPKTFGFFVVSD

Sbjct: 421 KKIYSYILTPEGGQLTSQKVLLNGKELNLXSDQLPQLNADESKTSFTLSPKTFGFFVVSD 480

Query: 481 ANVEACKK 488 ANVEACKK Sbjct: 481 ANVEACKK 488